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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 17, 2003, 11:18:03 ; Search time 1404.05 Seconds
(without alignments)
12007.805 Million cell updates/sec

Title: US-09-807-933B-12
Perfect score: 1041
Sequence: 1 atgaagttctccatcatcgcc.....ctggtgcgagcgaagtaa 1041

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estnu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hic:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_hic:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	gb_gss:*
18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pln:*
21:	em_gss_vrt:*
22:	em_gss_fun:*
23:	em_gss_mam:*
24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
27:	em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163.2	15.7	691	10	BES85661
2	115.8	11.1	450	13	BI200729
3	111	10.7	972	17	CNS02QMI
4	107	10.3	540	17	AZ583039
5	106.4	10.2	723	17	AZ627893
6	106.2	10.2	444	13	BI190695

7	103.8	10.0	498	17	AQ927406
8	103.4	9.9	597	17	AQ2764733
9	102.4	9.8	400	17	AZ000660
10	102.2	9.8	769	17	AG077414
11	102	9.8	279	17	CNS03W9F
12	101	9.7	810	17	CNS0272N
13	100.6	9.7	536	17	CNS03QOK
14	98.8	9.5	426	13	BI187295
15	98.2	9.4	529	17	AQ759124
16	97.8	9.4	708	17	AZ938145
17	97.4	9.4	408	9	AA484400
18	97	9.3	522	13	BI783235
19	96.6	9.3	630	17	CNS04HMV
20	96	9.2	447	17	BH094533
21	95.8	9.2	325	17	CNS03PK8
22	95.6	9.2	590	17	CNS03M2Z
23	94	9.0	745	17	BH500565
24	93.4	9.0	303	9	AA613152
25	92.4	8.9	998	17	BH133989
26	92.2	8.7	772	17	CNS02CCA
27	89.8	8.6	868	17	BH162606
28	89	8.5	512	13	EM034492
29	88.8	8.5	695	17	AZ262582
30	88.6	8.5	790	17	CNS0379X
31	88.4	8.5	511	17	AQ487936
32	87.8	8.4	284	17	CNS024VK
33	87.4	8.4	572	17	CNS043SN
34	87.4	8.4	723	17	AZ966297
35	87.2	8.4	774	17	CNS02APC
36	87.2	8.4	876	17	BH161693
37	86.8	8.3	884	17	CNS02NX2
38	86.6	8.3	703	17	AZ986572
39	86.4	8.3	330	14	D16000
40	86.4	8.3	426	14	D22721
41	86	8.3	821	17	CNS03F7F
42	85.8	8.2	329	9	AI668748
43	85.4	8.2	442	14	BQ622552
44	85.2	8.2	265	14	BQ985384
45	85	8.2	712	17	CNS04AL2

ALIGNMENTS

RESULT 1
BES85661
LOCUS
DEFINITION
BES85661 691 bp mRNA linear EST 17-AUG-2000
EST#6PSP6_D02_d2_014 KSU wheat Fusarium graminearum infected spike
CDNA library Triticum aestivum cDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BES85661 GI:9838604
EST.
Triticum aestivum
bread wheat.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BES85661 EST#6PSP6_D02_d2_014 KSU wheat Fusarium graminearum infected spike
CDNA library Triticum aestivum cDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.
BES85661 GI:9838604
EST.
Triticum aestivum
bread wheat.
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 691)
Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike cDNA library
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20
Seq primer: SP6

FEATURES

source
Location/Qualifiers
1..691
/organism="Triticum aestivum"
/cultivar="Sumai3"
/db xref="taxon:4565"
/clone="EST#GPS6 D02 d2_014"
/clone_lib="KSU wheat Fusarium graminearum infected spike cDNA library"
/tissue_type="Spike"
/dev_stage="Adult plant"
/lab_host="E. coli JM109"
/note="Vector: pCEM-T easy; Site 1: SacII; Site 2: SpeI; plants were grown in the greenhouse. Spikes were sprayed with Fusarium graminearum (at what stage). Total RNA, and poly(A) RNA were prepared from infected spikes. cDNA was prepared using the SmartTM PCR cDNA synthesis kit from Clontech. cDNA was cloned into the pCEM-T easy vector from Promega."

BASE COUNT 135 a 196 c 163 g 197 t

Query Match 15.7%; Score 163.2; DB 10; Length 691;
Best Local Similarity 60.8%; Pred. No. 5.3e-26;
Matches 322; Conservative 0; Mismatches 198; Indels 10; Gaps 3;

QY 424 TCTGGAAACGGTCGCACTACCGCTACTGGGATGTGCAAGCCCTCTTCGCGCTGGAC 483
DB 168 TCTGGAAAGTGGTCACTACTCGGATCTGGGACTGGCAAGCCCTCTTCGCTTGGAGT 227
QY 484 GGAAGAGCTTCTGTAACTAAGCCCTGTACTCACCTGTGCC---AAGATGTTGTGACGCGT 540
DB 228 GGCAGGCAAGTCAGCGCCCTGCTTGTGCTTGACAAAGAACACACCCCATCACT 287
QY 541 CTCGGTTCCGATGTCAGAGCGGTTGCTCGGGCCAGCGCTACATGTGCATGACAAC 600
DB 288 AACCTGAACGCGTCAACGGTTGTGAGAGTGGTGTCTGCGCTTGTGCTTACTTAACATC 347
QY 601 CAGCCCTGGGTTGCAATGACGACCTTGCTACGGTTTCTGCTGCGCACTTCGGTACG 660
DB 348 TCCCTTGGGCTGTCACAGACGACCTTGCTTACGGTTTCTGCTTACCAAGCTTGTGGT 407
QY 661 GCCGGTGCCTCTGCAITCTGCTGCGGTGTATCGAGCTTACCTTCAACACACTGCTGTC 720
DB 408 GGCACCTGAGACCACTGGTGTGCTGTGCTGTATGCTCTCACTTTCAGACCGGTCCGTA 467
QY 721 GCTGGCAAGAGTTTGTGCTCAGGTCAACCAACCGGTGATGATCTCAGCACCACCAAC 780
DB 468 AAGGGAAGAAGATGATGTTCAGTCCACCAACACTGGTGTGATCTCGGTGATACCC 527
QY 781 TTTCATTTGAGATGCCCGGGTGTGCTGGCTTACTTCAAGCTGCCAGTCCAGTGG 840
DB 528 TTTCACCTTATGATGCCCGGGTGTGCTGGTATATTCGATGATGACCTCTGAGTTC 587
QY 841 AACACCAACACCGATGCTGGGGTGTGCTGCTATGGCGGTATTAGCTCTATTTCAGAGTGC 900
DB 588 GGCAAGCCCTCG-----GTGGTGTCTCAGTACGGCGGCA-TCTCTTTCGAGGCCATGT 640
QY 901 GACAGCTTCTACCCAGTGTGAGGCTGGTTCGAGTGGAGATTCGATG 950
DB 641 GACAGTTTCCCGAGCTGCTCAAGGATGGTTCGCACTGGCGACTG 690

RESULT 2

BI200729 450 bp mRNA linear EST 10-JUL-2001
LOCUS olf05f5.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone olf05f5 5', mRNA
sequence.
BI200729
ACCESSION BI200729.1 GI:14666701
VERSION
KEYWORDS

SOURCE

ORGANISM
Fusarium sporotrichioides
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE
1 (bases 1 to 450)
AUTHORS Ren.Q., Tag.A., Peplow.A., Lai.H., Kupfer.C., Peterson.A., Beremand
M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability included
is the best homolog from a blastx search of Genbank nr 04-09-01
633 5e-66 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3
High quality sequence stop: 440.

FEATURES

source
Location/Qualifiers
1..450
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db xref="taxon:5514"
/clone="olf05f5"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 90 a 125 c 102 g 133 t
ORIGIN

Query Match 11.1%; Score 115.8; DB 13; Length 450;
Best Local Similarity 62.4%; Pred. No. 1.5e-15;
Matches 199; Conservative 0; Mismatches 117; Indels 3; Gaps 1;
QY 424 TCTGGAAACGGTCGCACTACCGCTACTGGGATGTGCAAGCCCTCTTCGCGCTGGAC 483
DB 132 TCTGGAAAGTGGGCACTCTACTCGGATCTGGGACTGGCAAGCCCTCTTCGCTTGGAGC 191
QY 484 GGAAGAGCTTCTGTAACTAAGCCCTGTACTCACCTGTGCAAGGATGCTGTC---AGCCGT 540
DB 192 GGCAGGCTAAAGTCAAGCGCCCTGCTCTGACTTGTGACAAACAAAGATACCTATCACT 251
QY 541 CTCGGTTCCGATGTCAGAGCGGTTGCTCGGGCCAGCGCTACATGTGCATGACAAC 600
DB 252 AACCTGAACGCTGTCAACCGTTGTGAGGGTGGTGTCTGCTTATGCTTGCACCAACTAC 311
QY 601 CAGCCCTGGTGTCTCAATGACGACCTTGTCTACGGTTTGTGCTGCTGCGAGTCTCGGTAGC 660
DB 312 TCCCGTGGGCTGTCAACGACGACCTTGTCTACGGTTTGTGCTGCTACCAAGCTTGTGCT 371
QY 661 GCGGGTGCCTCTGCACTTCTGCTCGGCTGTTCAGAGCTTACCTTCAACCAACATGCTGTC 720
DB 372 GGTAGTGAGGCCAGCTGGTGTGCTGTGCTATGCTCTACCTTTCACGACCGGTCGCGTG 431
QY 721 GCTGGCAAGAGTTTGTGCG 739
DB 432 AAGGGCAAGAAGATGATTG 450

RESULT 3

CNS02QMI/c 972 bp DNA linear GSS 14-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 158119 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL209475
ACCESSION AL209475.1 GI:7868294
VERSION

Db	331	ACACCACTATACACCA	CCACCA	CCAGCACC	ACCACTATATACCA	CCACCA	CCACCA	CCAGCACC	390	
Qy	319	ACTACTACTACCA <th>CCACCA</th> <th>AGACACCA</th> <th>CCACCA</th> <th>CAAGACCA</th> <th>CCACCA</th> <th>CCACCA</th> <th>CCAGGCTGCACCA</th> <th>378</th>	CCACCA	AGACACCA	CCACCA	CAAGACCA	CCACCA	CCACCA	CCAGGCTGCACCA	378
Db	391	ACTATCA <th>CCACCA</th> <th>CCACCA</th> <th>CCAGCACC</th> <th>ACCACTATATACCA</th> <th>CCACCA</th> <th>CCACCA</th> <th>CCAGCACC</th> <th>450</th>	CCACCA	CCACCA	CCAGCACC	ACCACTATATACCA	CCACCA	CCACCA	CCAGCACC	450
Qy	379	ACCTCCTCTTCC <th>ACACCA</th> <th>CTGGCTAC</th> <th>AGCCCATTTCTGGTGGCTTCTCTGGA</th> <th>AAACGGTGCG</th> <th>438</th> <td></td> <td></td>	ACACCA	CTGGCTAC	AGCCCATTTCTGGTGGCTTCTCTGGA	AAACGGTGCG	438			
Db	451	ACTACA <th>CAACCA</th> <th>CCACCA</th> <th>CCACCA</th> <th>CCAGCACC</th> <th>CCACCA</th> <th>CCACCA</th> <th>CCAGCACC</th> <th>510</th>	CAACCA	CCACCA	CCACCA	CCAGCACC	CCACCA	CCACCA	CCAGCACC	510
Qy	439	ACTACCGCTTAC <th>450</th> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	450							
Db	511	ACCACCA <th>CAAC</th> <th>522</th> <td></td> <td></td> <td></td> <td></td> <td></td>	CAAC	522						
RESULT 6										
BI190695										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
TITLE										
JOURNAL										
COMMENT										
FEATURES										
source										
BASE COUNT										
ORIGIN										
Query Match										
Best Local Similarity										
Matches 181;										
Qy	424	TTTGGAAACGGT	CGCAGCTAC	CCCTACTGGGATGTCTGCAAGCCCTCTTGGCTGGAC	48					
Db	158	TTCTGGAAGT	GGCCACTCTACTCGATACTGGGACTGTCTGCAAGCCCTCTTGTCTTGGAGC	21						
Qy	484	GGAAAGCTTCTCT	TAACCTAGCCCTGTACTCACCTGTGCCAAGGATGGTGTCTCTGAC	140						
Db	218	GGCAAGGCTAAGT	CAGCGCCCTGTCTGCTGAC	140						
Qy	541	CTCGGTTCCGAT	GTCCAGAGCGGTGGCTGGCGGCCAGCGCTACATGTGCAATGACAAC	600						

[illegible]

and selected for ampicillin resistance."

```
BASE COUNT      196 a      216 c      75 g      110 t
ORIGIN
Query Match      9.9%; Score 103.4; DB 17; Length 597;
Best Local Similarity 68.4%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 143; Conservative 0; Mismatches 66;
QY 203 CCAGAGCCACCCACCCACCCACCAAGGCTCCCACTACCAAGGCTCTCTGTGACCA 262
Db 335 CCAGAGCCACCCACCCACCCACCAAGGCTCCCACTACCAAGGCTCTCTGTGACCA 394
QY 263 CCACCAAGGCGCCACCCACCCACCAAGGCTCTCTGTGACCAAGGCGCCACTA 322
Db 395 CCACCAAGGCGCCACCCACCCACCAAGGCTCTCTGTGACCAAGGCGCCACTA 454
QY 323 CTACTACCAAGGCGCCACCCACCCACCAAGGCTCTCTGTGACCAAGGCGCCACT 382
Db 455 CCACCAAGGCGCCACCCACCCACCAAGGCTCTCTGTGACCAAGGCGCCACT 514
QY 383 CCTCTTCCAACTGGCTACAGCCCAT 411
Db 515 CCACCAAGGCGCCACCCACCCACCAAGGCTCTCTGTGACCAAGGCGCCACT 543
```

```
RESULT 9
LOCUS      AZ000660      400 bp      DNA      linear      GSS 24-FEB-2000
DEFINITION RPCI-23-313D18.TJ RPCI-23 Mus musculus genomic clone RPCI-23-313D18
ACCESSION  AZ000660
VERSION     AZ000660.1 GI:7075756
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1. (bases 1 to 400)
AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
          ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
          and Fraser,C.M.
TITLE      Mouse BAC End Sequences from Library RPCI-23
JOURNAL    Unpublished (1999)
COMMENT    Contact: Shaying Zhao
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: szhao@tigr.org
          Clones are derived from the mouse BAC library RPCI-23. For BAC
          library availability, please contact Pieter de Jong
          (pieter@dejong.med.buffalo.edu). Clones may be purchased from
          BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
          or from Resea ch Genetics (info@resgen.com). BAC end page:
          http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
          Plate: 313 row: D column: 18
          Seq primer: SP6
          Class: BAC ends.
FEATURES   Location/Qualifiers
            source      1..400
                        /organism="Mus musculus"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="RPCI-23-313D18"
                        /clone_lib="RPCI-23"
                        /sex="Female"
                        /lab_host="DH10B"
                        /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1:
                        EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
                        brain genomic DNA was isolated and partially digested
                        with a combination of EcoRI and EcoRI Methylase. Size
                        selected DNA was cloned into the pBACe3.6 vector at the
```

EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "

```
BASE COUNT      151 a      171 c      26 g      52 t
ORIGIN
Query Match      9.8%; Score 102.4; DB 17; Length 400;
Best Local Similarity 64.2%; Pred. No. 1.4e-12; Indels 0; Gaps 0;
Matches 154; Conservative 0; Mismatches 86;
QY 175 ATCCCAAGGCTCAAGTCCAGGTAACCCCAAGACCAACCAACCAAGGCT 234
Db 134 ATCCCAAGGCTCAAGTCCAGGTAACCCCAAGACCAACCAACCAAGGCT 193
QY 235 GCCACTACCAACCAAGGCTCTGTGACCAACCAACCAAGGCTCTGTGACCAACCAAG 294
Db 194 ATCCCAAGGCTCAAGTCCAGGTAACCCCAAGACCAACCAACCAAGGCT 253
QY 295 GCCCTGTGACCAACCAAGGCTCTGTGACCAACCAACCAAGGCTCTGTGACCAACCAAG 354
Db 254 ACCATCATCAGCAACCAACCAAGGCTCTGTGACCAACCAACCAAGGCTCTGTGACCAACCAAG 313
QY 355 ACCCAACCAAGGCTGACCAACCAACCAAGGCTCTGTGACCAACCAACCAAGGCTCTGTGACCAACCAAG 414
Db 314 ATCTCCACCAACCAAGGCTGACCAACCAACCAAGGCTCTGTGACCAACCAACCAAGGCTCTGTGACCAACCAAG 373
```

```
RESULT 10
LOCUS      AG077414      769 bp      DNA      linear      GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-071015.R, genomic survey sequence.
ACCESSION  AG077414
VERSION     AG077414.1 GI:16629216
KEYWORDS   GSS.
SOURCE     Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
          BAC Library Clone:PTB-071015.R.
ORGANISM   Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE  1
AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of Library PTB
JOURNAL    Unpublished
COMMENT    2 (bases 1 to 769)
          Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Totoki,Y., Watanabe,H. and Sakaki,Y.
          Direct Submission
          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          1-7-22 Suehiro-chou,Tsukuba-shi,Ibaraki-city,305-8565, Japan
          (E-mail:chimps@gs.c.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
          Tel:81-45-503-9111, Fax:81-45-503-9170)
          Clones are derived from the chimpanzee BAC library PTB This BAC end
          was generated during the R&D process and may have higher chance of
          clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector      : pKS145
R.Site 1    : SacI
R.Site 2    : SacI.
FEATURES   Location/Qualifiers
            source      1..769
                        /organism="Pan troglodytes"
                        /db_xref="taxon:9598"
                        /clone="PTB-071015.R"
                        /sex="male"
                        /cell_type="lymphoblast"
                        /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT  201 a      329 c      72 g      167 t
ORIGIN
Query Match      9.8%; Score 102.2; DB 17; Length 769;
```


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